Genetic stock structure of *Chrysoblephus puniceus* in the South West Indian Ocean

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Introduction
- Most important commercial linefish species in Kwa-zulu Natal (South Africa) and southern Mozambique.
- Historically been managed as two stocks separated by a political boundary.
- Need to assess the levels of connectivity through *C. puniceus* distribution to determine the trans boundary nature of the stock and the correct number of management units.

Hypothesis
- $H_0$: There are high levels of gene flow with one population throughout *C. puniceus* distribution range.

Materials and Methods
- Genetic samples for extractions were collected throughout *C. puniceus* distribution.
- The mitochondrial control region was sequenced following Teske et al. 2010.
- 10 microsatellite loci were amplified following Chopelet et al. 2009.
- Several genetic diversity, connectivity and population structure analyses were done.

Results: Sampling
- High haplotype diversity = 0.97.
- Haplotype network had a lot of shared haplotypes (figure 2).

Results: mtDNA
- Overall 282 viable 300bp mtDNA control region sequences.
- 284 individual microsatellite datasets with 10 loci.

Results: Microsatellites
- No significant departure from HWE except for two loci.
- Allelic richness was consistent between sampling sites.
- No significant trends with linkage disequilibrium.
- Pairwise comparisons indicate no genetic differences for either tests (table 2).

Discussion
- mtDNA revealed some significant structuring around Xai Xai and Inhaca that could be associated with an upwelling cell.
- Overall mtDNA and microsatellites indicate a single population of *C. puniceus*.
- Migrate-n indicates that ocean currents may facilitate larval movement or dispersal.
- No significant trend in spatial autocorrelation were observed.

Acknowledgements
- SWIOFP, WIDMSA and DADDD for project and bursary support; ORI and DAFF for samples from South Africa; IIP (Mozambique) and Rui Jorge Mutombene for assistance in obtaining Mozambique samples.